

L Number	Hits	Search Text	DB	Time stamp
1	2	5955309.pn.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/08/31 11:04
2	2	5874243.pn.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/08/31 11:05
3	2	6043054.pn.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/08/31 11:05
4	2	5976834.pn.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/08/31 11:06
5	2	5955308.pn.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/08/31 11:06
6	2	6048711.pn.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/08/31 11:06
-	2	6262246.pn.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/08/31 11:04
-	13	gerald-christophe-p-g.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/10/01 12:40
-	38	jones-kenneth-a.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/10/01 12:40
-	19	bonini-james-a.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/10/01 12:41
-	16	borowsky-beth.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/10/01 12:41
-	13	npff adj receptor	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/10/01 12:41

## 09866248 Results

SEQ ID NO: 6

Result No.	Score	Query Match	Length	DB	ID	Description
1	2208	100.0	420	2	AAW81358	Aaw81358 Human 7-t
2	2208	100.0	420	3	AAY79375	Aay79375 Human neu
3	2208	100.0	420	3	AAY99930	Aay99930 HLWAR77 p
4	2208	100.0	420	4	AAU00233	Aau00233 Orphan re
5	2208	100.0	420	5	AAU79013	Aau79013 Human G p
6	2208	100.0	522	4	ABB11723	Abb11723 Human GPC
7	2208	100.0	522	7	ADC89684	Adc89684 Human neu
8	2204	99.8	420	3	AAB07426	Aab07426 Amino aci
9	2204	99.8	522	4	AAU00234	Aau00234 Orphan re
10	2204	99.8	522	6	ABG73522	Abg73522 Human G-p
11	2204	99.8	522	6	ABP82012	Abp82012 Human neu
12	2115	95.8	408	3	AAY76882	Aay76882 Human NPY
13	1730.5	78.4	417	3	AAY79377	Aay79377 Rat neuro
14	1719	77.9	332	4	AAU18133	Aau18133 Novel hum
15	1719	77.9	332	4	AAU18688	Aau18688 Renal and
16	1719	77.9	332	4	AAU21718	Aau21718 Novel hum

Result No.	Score	Query Match	Length	DB	ID	Description
1	2208	100.0	420	3	US-09-255-368-6	Sequence 6, Appli
2	1060	48.0	430	3	US-09-255-368-8	Sequence 8, Appli
3	1024	46.4	432	3	US-09-255-368-2	Sequence 2, Appli
4	525.5	23.8	444	3	US-09-119-788-2	Sequence 2, Appli
5	525.5	23.8	444	4	US-09-426-290-2	Sequence 2, Appli
6	499.5	22.6	402	3	US-08-846-704-4	Sequence 4, Appli
7	499.5	22.6	402	4	US-08-462-509B-2	Sequence 2, Appli
8	499.5	22.6	402	5	PCT-US95-05616-2	Sequence 2, Appli
9	499.5	22.6	425	3	US-08-846-704-2	Sequence 2, Appli
10	499.5	22.6	425	4	US-09-479-128-2	Sequence 2, Appli
11	499.5	22.6	425	4	US-09-211-823C-22	Sequence 22, Appl
12	476.5	21.6	369	4	US-08-462-509B-4	Sequence 4, Appli

## RESULT 1

US-09-255-368-6

; Sequence 6, Application US/09255368

; Patent No. 6262246

; GENERAL INFORMATION:

; APPLICANT: Gerald, Christophe P.G.

; APPLICANT: Jones, Kenneth A.

; APPLICANT: Bonini, James A.

; APPLICANT: Borowsky, Beth

; TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide FF (NPFF) Receptors

; TITLE OF INVENTION: and Uses Thereof

; FILE REFERENCE: 1795/57155-A

; CURRENT APPLICATION NUMBER: US/09/255,368

; CURRENT FILING DATE: 1999-02-22

; EARLIER APPLICATION NUMBER: 09/161,113

; EARLIER FILING DATE: 1998-09-25

; NUMBER OF SEQ ID NOS: 42

; SOFTWARE: PatentIn Ver. 2.0 - beta

; SEQ ID NO 6

; LENGTH: 420

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-255-368-6

Query Match 100.0%; Score 2208; DB 3; Length 420;  
Best Local Similarity 100.0%; Pred. No. 2.4e-200;  
Matches 420; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNEKWDNTSSSENWHPIWNVNDTKHHLYSDINITYVNYLHQPQVAAIFIISYFLIFFLCM 60  
|||||

```

Db      1 MNEKWDNTSSSENWHPIWNVNDTKHHLYSDINITYVNYLHQPVAAIFIISYFLIFFLCM 60
Qy      61 MGNTVVCFIVMRNKHMTVTNLFILNLAISDLLVGIFCMPITLLDNIIAGWPFGNTMCKI 120
      |||
Db      61 MGNTVVCFIVMRNKHMTVTNLFILNLAISDLLVGIFCMPITLLDNIIAGWPFGNTMCKI 120
Qy      121 SGLVQGISVAASVFTLVIAIAVDRFQCVVYPFKPKLTIKTAFAVIIMIIWVLAITIMSPSAV 180
      |||
Db      121 SGLVQGISVAASVFTLVIAIAVDRFQCVVYPFKPKLTIKTAFAVIIMIIWVLAITIMSPSAV 180
Qy      181 MLHVQEEKYYRRLNSQNKTSPVYWCREDWPNQEMRKIYTTVLFANIYLAPLSLIVIMYG 240
      |||
Db      181 MLHVQEEKYYRRLNSQNKTSPVYWCREDWPNQEMRKIYTTVLFANIYLAPLSLIVIMYG 240
Qy      241 RIGISLFRAAVPHTGRKNQEQWHVVSRRKKQKIIKMLLIVALLFILSWLPLWTLMLMSDYA 300
      |||
Db      241 RIGISLFRAAVPHTGRKNQEQWHVVSRRKKQKIIKMLLIVALLFILSWLPLWTLMLMSDYA 300
Qy      301 DLSPNELQIINIYYIPFAHWLAFGNSSVNPPIYGFFNENFRRGFQEAFLQLCQKRAKPM 360
      |||
Db      301 DLSPNELQIINIYYIPFAHWLAFGNSSVNPPIYGFFNENFRRGFQEAFLQLCQKRAKPM 360
Qy      361 EAYALKAKSHVLINTSNQLVQESTFQNPHGSETLLYRKSAEKPQQELVMEELKETTNSSEI 420
      |||
Db      361 EAYALKAKSHVLINTSNQLVQESTFQNPHGSETLLYRKSAEKPQQELVMEELKETTNSSEI

```

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	485.5	22.0	449	2	A41738	neuropeptide Y rec
2	480	21.7	423	2	B40470	glucocorticoid-ind
3	465	21.1	381	2	I39187	neuropeptide Y/pep
4	460	20.8	443	2	D40470	glucocorticoid-ind
5	445.5	20.2	444	2	A42685	cholecystokinin re
6	444.5	20.1	384	2	A45490	neuropeptide Y/pep
7	444	20.1	382	2	B46133	neuropeptide Y/pep
8	443.5	20.1	349	2	S12863	G protein-coupled
9	443	20.1	428	2	JN0692	cholecystokinin ty
10	437	19.8	382	2	S27388	neuropeptide Y rec
11	437	19.8	491	2	C40470	glucocorticoid-ind
12	436	19.7	436	2	JC5599	cholecystokinin-A
13	435	19.7	370	1	I52315	G protein-coupled

#### RESULT 1

A41738  
neuropeptide Y receptor - fruit fly (*Drosophila melanogaster*)  
N;Alternate names: G protein-coupled receptor PR4  
C;Species: *Drosophila melanogaster*  
C;Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 20-Apr-2000  
C;Accession: A41738  
R;Li, X.J.; Wu, Y.N.; North, R.A.; Forte, M.  
J. Biol. Chem. 267, 9-12, 1992  
A;Title: Cloning, functional expression, and developmental regulation of a neuropeptide Y receptor from *Drosophila melanogaster*.  
A;Reference number: A41738; MUID:92112730; PMID:1370455  
A;Accession: A41738  
A;Molecule type: mRNA  
A;Residues: 1-449 <LIA>  
A;Cross-references: GB:M81490; NID:g157996; PIDN:AAA28727.1; PID:g157997  
C;Genetics:  
A;Gene: FlyBase:NepYr  
A;Cross-references: FlyBase:FBgn0004842  
C;Superfamily: neurokinin 1 receptor  
C;Keywords: appetite; G protein-coupled receptor; transmembrane protein

Query Match 22.0%; Score 485.5; DB 2; Length 449;  
Best Local Similarity 34.3%; Pred. No. 1.4e-32;

Matches	107;	Conservative	52;	Mismatches	114;	Indels	39;	Gaps	7;
Qy	49	IISYFL---IFFLCMMGNITVVC	FIVMRNKHMTVTNLFILNL	ASIDLLVGIFC	MPTLLD				105
			:	:	:	:	:	:	
Db	91	IIVYMLYIPIFIFALIGNGT	VCYIVYSTPRMRTVTNYFI	ASLAIGDILMSFF	CEPSSFIS				150
Qy	106	NIIAG-WPFGNTMKCKISGLV	QGISVAASVFTLV	IAIVDRFCQCVVYPFKPKL	TIKTA	FVII			164
			:	:	:	:	:	:	
Db	151	LFILNYWPFGLALCHFVNYS	QAVSVLVSAITLVAISID	RYAIAIMWPLKPRIT	KRYATFII				210
Qy	165	MIIVLVAITIMSPSAVM-----	LHVQEEKYRVL	NSQNKTSPVYWC	REDWPNQEM				215
		:	:	:	:	:	:	:	
Db	211	AGVWFIALATALPIPIVSG	LIDIPMS	PWHTKCEKYI-----	CREMWPSRSQ				255
Qy	216	RKIYTTVLFANIYLA	PLSLIVIMYGRIGISL	FRAAVPHTGRKNQE	QWHVVS	RKKQKIIKM			275
			:	:	:	:	:	:	
Db	256	EYYYTSLSLFALQFV	VPLGVLI	FITYARITIRVWAKRPP	GEAETNRDQ--	RMARSKRKMVKM			313
Qy	276	LLIVALLFILSWLPL	WTLMML---SDYADL	SPNELQIINIYIYP	FAHWLAF	GNSSVNPII			332
		:	:	:	:	:	:	:	
Db	314	MLTVIVVFTCCWLP	FNILQQLLNDEE	FAHWDPLP-----	YVWFAFHWL	AMSHCCYNPII			367
Qy	333	YGFFNFENFR	RGF						344
		:							
Db	368	YCYMNARFR	SGF						379

## RESULT 1

RL J. Biol. Chem. 275:25965-25971(2000).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM 2), AND CHARACTERIZATION.  
 RC TISSUE=Spinal cord;  
 RX MEDLINE=20564301; PubMed=11024015;  
 RA Bonini J.A., Jones K.A., Adham N., Forray C., Artymyshyn R.,  
 RA Durkin M.M., Smith K.E., Tamm J.A., Boteju L.W., Lakhani P.P.,  
 RA Raddatz R., Yao W.-J., Ogozalek K.L., Boyle N., Kouranova E.V.,  
 RA Quan Y., Vaysse P.J., Wetzel J.M., Branchek T.A., Gerald C.,  
 RA Borowsky B.;  
 RT "Identification and characterization of two G protein-coupled  
 RT receptors for neuropeptide FF.";  
 RL J. Biol. Chem. 275:39324-39331(2000).  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORM 3).  
 RX MEDLINE=20299143; PubMed=10837915;  
 RA Parker R.M.C., Copeland N.G., Eyre H.J., Liu M., Gilbert D.J.,  
 RA Crawford J., Couzens M., Sutherland G.R., Jenkins N.A., Herzog H.;  
 RT "Molecular cloning and characterisation of GPR74 a novel G-protein  
 RT coupled receptor closest related to the Y-receptor family.";  
 RL Brain Res. Mol. Brain Res. 77:199-208(2000).  
 RN [5]  
 RP SEQUENCE FROM N.A. (ISOFORM 2).  
 RA Liu Q., Guan X.-M., McDonald T.P., Jiang Q., Zeng Z., Marlene J.,  
 RA Williams D.L. Jr., Hong Y., Figueroa D., Clements M.K., Mallee J.,  
 RA Wang R., Evans J., Gould R., Austin C.P.;  
 RT "Identification and characterization of two cognate receptors for  
 RT mammalian FMRFamide-like neuropeptides.";  
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP SEQUENCE FROM N.A. (ISOFORM 4).  
 RA Laemmle B.S., Schindler M., Beilmann M., Hamilton B.S., Doods H.N.,  
 RA Wieland H.A.;  
 RT "Cloning and characterization of the NPGP receptor and identification  
 RT of a novel short mRNA isoform in human hypothalamus.";  
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Receptor for NPAF (A-18-F-amide) and NPFF (F-8-F-amide)  
 CC neuropeptides, also known as morphine-modulating peptides. Can  
 CC also be activated by a variety of naturally occurring or synthetic  
 CC FMRF-amide like ligands. This receptor mediates its action by  
 CC association with G proteins that activate a phosphatidylinositol-  
 CC calcium second messenger system.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=4;  
 CC Comment=Experimental confirmation may be lacking for some  
 CC isoforms;  
 CC Name=1; Synonyms=long form;  
 CC IsoId=Q9Y5X5-1; Sequence=Displayed;  
 CC Name=2; Synonyms=short form;  
 CC IsoId=Q9Y5X5-2; Sequence=VSP\_001907;  
 CC Name=3;  
 CC IsoId=Q9Y5X5-3; Sequence=VSP\_001908, VSP\_001909;  
 CC Name=4;  
 CC IsoId=Q9Y5X5-4; Sequence=VSP\_001910, VSP\_001911;  
 CC -!- TISSUE SPECIFICITY: Isoform 1 is abundant in placenta. Relatively  
 CC highly expressed in thymus, testis, and small intestine. Expressed  
 CC at low levels in several tissues including spleen, prostate,  
 CC brain, heart, ovary, colon, kidney, lung, liver and pancreas and  
 CC not expressed in skeletal muscle and leukocytes. Highest but  
 CC relatively low level of isoform 2 in placenta and very low level  
 CC in numerous tissues including adipose tissue and many brain  
 CC regions. Isoform 3 is expressed in brain and heart and, at lower  
 CC levels, in kidney, liver, lung and pancreas.  
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 CC HIGHEST TO OREXIN, NPY AND CHOLECYSTOKININ RECEPTORS.  
 CC -!- CAUTION: Ref.4 sequence differs from that shown due to a  
 CC frameshift in position 503.  
 CC -----  
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 CC -----

DR EMBL; AF119815; AAD22047.1; -.  
 DR EMBL; AF257210; AAF87078.1; -.  
 DR EMBL; AF268899; AAG41398.1; -.  
 DR EMBL; AF236083; AAK58513.1; ALT\_FRAME.  
 DR EMBL; AF330053; AAK94197.1; -.  
 DR EMBL; AJ311393; CAC85427.1; -.  
 DR Genew; HGNC:4525; GPR74.  
 DR MIM; 607449; -.  
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.  
 DR GO; GO:0004930; F:G-protein coupled receptor activity; TAS.  
 DR GO; GO:0008151; P:cell growth and/or maintenance; TAS.  
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.  
 DR GO; GO:0009582; P:perception of abiotic stimulus; TAS.  
 DR InterPro; IPR000276; GPCR\_Rhodopsn.  
 DR InterPro; IPR005395; NPFF\_receptor.  
 DR InterPro; IPR005397; NPFF\_receptor2.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PR00237; GPCRRHODOPSN.  
 DR PRINTS; PR01570; NPFFRECEPTOR.  
 DR PRINTS; PR01572; NPFFRECEPTR2.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS00262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;  
 KW Alternative splicing.  
 FT DOMAIN 1 147 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 148 168 1 (POTENTIAL).  
 FT DOMAIN 169 184 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 185 205 2 (POTENTIAL).  
 FT DOMAIN 206 221 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 222 242 3 (POTENTIAL).  
 FT DOMAIN 243 262 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 263 283 4 (POTENTIAL).  
 FT DOMAIN 284 319 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 320 340 5 (POTENTIAL).  
 FT DOMAIN 341 377 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 378 398 6 (POTENTIAL).  
 FT DOMAIN 399 413 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 414 434 7 (POTENTIAL).  
 FT DOMAIN 435 522 CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 220 308 BY SIMILARITY.  
 FT CARBOHYD 110 110 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 122 122 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 133 133 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 300 300 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT VARSPLIC 1 102 Missing (in isoform 2).  
 FT /FTId=VSP\_001907.  
 FT VARSPLIC 1 99 Missing (in isoform 3).  
 FT /FTId=VSP\_001908.  
 FT VARSPLIC 100 100 R -> M (in isoform 3).  
 FT /FTId=VSP\_001909.  
 FT VARSPLIC 101 132 FIMNEKWDNTSSSENWHPIWNVNDTKHHLYSDI -> MAIWK  
 FT HDVQDQWIGPGNICRSFSLYVSCNCCR (in isoform  
 FT 4).  
 FT /FTId=VSP\_001910.  
 FT VARSPLIC 133 522 Missing (in isoform 4).  
 FT /FTId=VSP\_001911.  
 FT CONFLICT 466 466 A -> T (IN REF. 1 AND 4).  
 SQ SEQUENCE 522 AA; 60270 MW; 40CB9FCD42F77041 CRC64;

Query Match 100.0%; Score 2208; DB 1; Length 522;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-136;  
 Matches 420; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNEKWDNTSSSENWHPIWNVNDTKHHLYSDINITYVNYLHQPQVAAIFIISYFLIFFLCM 60  
 |||

Db 103 MNEKWDTNSSSENWHPIWNVNDTKHHLYSDINITYVNYLHQPQVAAIFIISYFLIFFLCM 162

Qy 61 MGNTVVCFIVMRNKHMTVTNLFILNLAISDLLVGIFCMPITLLDNIIAGWPFPGNTMCKI 120  
 |||

Db 163 MGNTVVCFIVMRNKHMTVTNLFILNLAISDLLVGIFCMPITLLDNIIAGWPFPGNTMCKI 222

Qy 121 SGLVQGISVAASVFTLVIAVDRFQCQVVPFKPKLTIKTAFTVIIMIIVWLAITIMSPSAV 180  
 |||

Db 223 SGLVQGISVAASVFTLVIAVDRFQCQVVPFKPKLTIKTAFTVIIMIIVWLAITIMSPSAV 282

Qy 181 MLHVQEEKYYRVRLNSQNKTSVPVYWCREDWPNQEMRKIYTTVLFANIYLAPLSLIVIMYG 240  
 |||

Db 283 MLHVQEEKYYRVRLNSQNKTSVPVYWCREDWPNQEMRKIYTTVLFANIYLAPLSLIVIMYG 342

Qy 241 RIGISLFRAAVPHTGRKNQEQWHVVSRRKKQKIIKMLLIVALLFILSWLPLWTLMMLSDYA 300  
 |||

Db 343 RIGISLFRAAVPHTGRKNQEQWHVVSRRKKQKIIKMLLIVALLFILSWLPLWTLMMLSDYA 402

Qy 301 DLSPNELQIINIYIYPFAHWLAFGNSSVNPPIYGFFNENFRRGFQEAFLQLCQKRAKPM 360  
 |||

Db 403 DLSPNELQIINIYIYPFAHWLAFGNSSVNPPIYGFFNENFRRGFQEAFLQLCQKRAKPM 462

Qy 361 EAYALKAKSHVLINTSNQLVQESTFQNPGETLLYRKSAEKPQQELVMEELKETTSNSEI 420  
 |||

Db 463 EAYALKAKSHVLINTSNQLVQESTFQNPGETLLYRKSAEKPQQELVMEELKETTSNSEI 522

Result No.	Score	Query			DB	ID	Description
		Match	Length				
1	1748.5	79.2	417	11	Q924H0		Q924h0 mus musculu
2	1748.5	79.2	417	11	Q8BKR6		Q8bkr6 mus musculu
3	1666	75.5	405	11	Q924N0		Q924n0 mus musculu
4	984	44.6	432	11	Q924G9		Q924g9 rattus norv
5	553	25.0	758	5	Q7YU49		Q7yu49 drosophila
6	499.5	22.6	425	4	Q9HBV6		Q9hbv6 homo sapien
7	487.5	22.1	449	5	Q9VB87		Q9vb87 drosophila
8	487	22.1	422	11	Q8VHD7		Q8vhd7 rattus norv
9	486.5	22.0	365	11	Q8BHH0		Q8bhh0 mus musculu
10	485	22.0	600	5	Q9VW75		Q9vw75 drosophila
11	476	21.6	402	5	Q964E5		Q964e5 dugesia tig
12	470.5	21.3	429	5	P92045		P92045 lymnaea sta
13	469.5	21.3	364	11	Q8BV78		Q8bv78 mus musculu
14	463.5	21.0	381	11	Q8BWV1		Q8bvw1 mus musculu
15	460.5	20.9	381	11	Q9ERC0		Q9erc0 rattus norv
16	455.5	20.6	540	5	Q9VRM0		Q9vrm0 drosophila
17	451.5	20.4	375	13	O57463		O57463 brachydanio